

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

gb|AF011751| (9599 letters)

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|2327070|gb|AF011751.1|AF011751

Description

Hepatitis C virus strain H77 pCV-H77C polyprotein gene, complete cds

Molecule type

nucleic acid

Query Length

9599

Subject ID

gi|5420376|emb|AJ238799.1|

Description

Hepatitis C virus type 1b complete genome, isolate Con1

Molecule type

nucleic acid

Subject Length

9605

Program

BLASTN 2.2.21+ [Citation](#)

Reference

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	28
Expect value	10
Hitlist size	100
Match/Mismatch scores	1,-2
Gapcosts	0,0
Low Complexity Filter	Yes
Filter string	L.m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.33271	1.28

K	0.620991	0.46
H	1.12409	0.85

Results Statistics

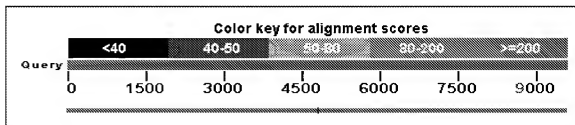
Effective search space 91853047

[Graphic Summary](#)

Distribution of 2 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[Dot Matrix View](#) **Plot of gi|2327070|gb|AF011751.1|AF011751 vs gi|5420376|emb|AJ238799.1| [?]**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

**Descriptions**

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

Sequence ID	Description	Length	Score	E-value	Identity
AJ238799.1	Hepatitis C virus type 1b complete genome, isolate Con1	5956	9311	99%	0.0 79%

Alignments **Select All** Get selected sequences Distance tree of results Multiple alignment **NEW**

>emb|AJ238799.1| Hepatitis C virus type 1b complete genome, isolate Con1
Length=9605

Sort alignments for this subject se
E value **Score** **Percent identity**
Query start position **Subject sta**

Score = 5956 bits (3225), Expect = 0.0
Identities = 7350/9298 (79%), Gaps = 458/9298 (4%)
Strand=Plus/Plus

Query	531	CCTATCCCCAAGGCACGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCCTGG	590
Sbjct	531	CCTATCCCCAAGGCTCGCCAGCCCGAGGGTAGGGCCTGGGCTCAGCCCGGGTACCCCTGG	590
Query	591	CCCCCTATATGGCAATAGGG-TTGGGGTGGGCGGATGGCTCCTGTCTCCCCGTGGCTC	649
Sbjct	591	CCCCCTATATGGCAATAGGGCTTG-GGGTGGGACGGATGGCTCCTGTACCCCGTGGCTC	649
Query	650	TCGGCCTAGCTGGGGCCCCACAGACCCCGGCGTAGGTCGCGCAATTGGGTAAGGTCAT	709
Sbjct	650	TCGGCCTAGTTGGGGCCCCACGGACCCCGGCGTAGGTCGCGCAATTGGGTAAGGTCAT	709
Query	710	CGATACCCCTACGTGCGGCTTCGCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC	769
Sbjct	710	CGATACCCCTACGTGCGGCTTCGCGCATCTCATGGGTACATTCGCTCGTCGGCGCCCC	769
Query	770	TCTTGGAGGCGCTGCCAGGGCCCTGGCGCATGGGCTCCGGGTTCTGGAAGACGGCGTGAA	829
Sbjct	770	CCTAGGGGCGCTGCCAGGGCCCTGGCGCATGGGCTCCGGGTTCTGGAAGACGGCGTGAA	829
Query	830	CTATGCAACAGGGAACCTTCCTGGTTGCT-CITTCCTATCTTCCTCTCGGCCCTGCTCT	888
Sbjct	830	CTATGCAACAGGGAATCTGCCGGTTGCTCCTTT-TCATCTTCCTTTTGCTTTGCTGT	888
Query	889	CTTGCTGACTGTGCCC-GCTTCAGCCTACCAAGTGCACAA--T-TCCTCGGGGCTTTAC	944
Sbjct	889	CCTGTTTGACCAT-CCCAGCTTCCGCTTATGAAGTGCACACGTAT-C-CGGAG-TGTAC	944
Query	945	CATGTACCAATGATTGC-CCTAACTCAGTATTGTGTACGAGGCGGCCG--ATGCCATC	1001
Sbjct	945	CATGTACGAAACGACTGTCC-AACGCAAGCATTGTGTATGAGGACGCGGACATG--ATC	1001
Query	1002	CTGCACACTCCGGGGTGTGT-CCCTTGCCTTCGCGAGGGTAACGCCTCGAGGTTGTGGGT	1060
Sbjct	1002	ATGCATACCCCGGGTGCCTGCC-TGCGTTTCGGGAGAACAACTCCTCCCGCTGCTGGGT	1060
Query	1061	GGCGGTGACCCACCGGTGGCCACCGAGGACGGCAAC-TCCCCACAACGCA-GCTTCGA	1118
Sbjct	1061	AGCGCTCACTCCACGCTCGCGGCCAGGAAC-GCTAGCGTCCCACTACG-ACGATACGA	1118
Query	1119	CGTCATATCGATCTGCTTGTGCGGAGC-GCCACCCTCTGCTCGGCCCTCTACGTGGGGGA	1177
Sbjct	1119	CGCCATGTCGATTGTCTGTTGGG-GCGGCTGCTCTGCTCCGCTATGTACGTGGGAGA	1177

Query	1178	CCTGTGCGGGTCTGTCTTT-CTTGTGGTCAACTGTTTACCTTCTCTCC-CAGGCGCCAC	1235
Sbjct	1178	TCTCTGCGGATCTGT-TTCTCTGCTCGCCAGCTGTTACCTTCTCGCCTC-GCCGCGAC	1235
Query	1236	TGGAGCAC-G--CAAGACTGCAATTGTTCTATCTATCCCGGCATATAACGGGTCATCGC	1292
Sbjct	1236	--GA-GACAGTACAGGACTGCAATTGCTCAATATATCCCGGCCAGTGACAGGTACCCGT	1292
Query	1293	ATGGCATGGGATATGATGATGAACCTGGTCCCCCTACGCGAGCGTTGGTGGTAGCTCAGCTG	1352
Sbjct	1293	ATGGCTTGGGATATGATGATGAACCTGGTCACTACAGCAGCCCTAGTGGTATCGAGTTA	1352
Query	1353	CTCCGGATCCCACAAGCCATCATGGACATGATCGTGGTCTCTACTGGGAGTCCCTGGCG	1412
Sbjct	1353	CTCCGGATCCCACAAGCTGCTGGGATATGGTGGCGGGGGCCATTGGGGAGTCTTAGGG	1412
Query	1413	GGCATAGCGTA-TTCTCCATGGTGGGGAACCTGGGCGAAGGTCCTGGTAGTGTCTGTCT	1471
Sbjct	1413	GGCCTTGCTACTAT-TCCATGGTGGGGAACCTGGGCTAAGGTTCTGATTGTGATGCTACT	1471
Query	1472	ATTGCGCGGCTGCGACGCGAAACCCACGTACCGGGGGAATGCCGGCC-GCACCCAGG	1530
Sbjct	1472	CTTTGCGCGGCTGTGACGGGGGAACCTATGTGACAGGGG-GACGATGCCCAAAACAC-C	1529
Query	1531	CT-GGGCTTGTGGT--CTCCTTACACCAGGCGCCA-AGCAGAACATCCAAC-TGATCAA	1585
Sbjct	1530	CTCGGG-AT-TACGTCCCTCTTTTACCCGG-GTCACTCCAGAAAATCCAGCTTG-TAAA	1585
Query	1586	CACCAACGGCAGTTGGCACATCAATAGCACGGCTTGAATTGCAATGAAGCCCTTAACAC	1645
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Query	1646	-CGGCTGGTTAGCAGGGCTCTTCTATC-AACACAAATCAACTCTTCAGGCTGCTCTGAG	1703
Sbjct	1646	TGGGTTCCCTT-GCTGCGCTGTTCTA-CGTGCACAAGTTCAACTCATCTGGATGCCAGAG	1703
Query	1704	AGGTTGGCCAGCTGCCGACGCC-T-TACCGATTITGCCAGGGCTGGGGTCCATCATGTT	1761
Sbjct	1704	CGCATGGCCAGCTGCAG-CCCATCGA-CGCGTTCTGCTAGGGGTGGGGGCCATCACTT	1761
Query	1762	ATGCCAACG-G--A-AGCGGCTC-GACGA-ACGCCCCCTACTGCTGGCACTACCTCCAA	1815
Sbjct	1762	A---CAATGAGTCACA-CAG-CTCGGACCAGA-GGCCTTATTGTTGGCACTACGACCCC	1815
Query	1816	GACCTTGCGCAATTGIGCCCGCAAAG-AGCGTGTGTGGCCCGGTATATTGCTTCACTCC	1874
Sbjct	1816	GGCCGTGCGGTATCGTACCOCGCGCGCAG-GTGTGTGGTCCAGTGTACTGCTTAC-CCC	1873
Query	1875	-AGCCCCGTGGTGGTGGGAACGACCGACAGG-TCGGGCG-CGCTACCTACAGCTGGGGT	1931
Sbjct	1874	AAGCCCTGTCTGGTGGGACGACCGACCGGTT-CGCGTC-CCTACGTACAGTGGGG-	1930
Query	1932	GCA-AATGATACGGATGT-CTTCGCTCTTAACAACAC-CAGGCCACCCTGGGCAATTGG	1988
Sbjct	1931	GGAGAATGAGACGGAGCTGTGC-TTCTTAACAACACGC-GGCCGCCCAAGGCAACTGG	1988
Query	1989	TTGCGTTGTACCTGGATGAACCTCA--ACTGGATTACCAAAG-TGTGC-GGAGCGCCCC	2044
Sbjct	1989	TTTGGCTGTACATGGATGAA-T-AGCACTGGGTTACAC-AAGACGTGGGGGGC-CCCC	2044
Query	2045	TTGTGTCATTCGGAGGGG-TGGGCAACAACCTTG-CTCTGCCCACTGATTGCTTCCG	2102
Sbjct	2045	GTGTAACATCGG-GGGGATCGGCAATAAAACCTTGAC-CTGCCCCACGGACTGCTTCCG	2102
Query	2103	AAACATCCGGAAGCCACATACTCTC-GGTGCGGCTCCGGTCCCTGGATT-ACACCCAGGT	2160
Sbjct	2103	AAGCACCCCGAGGCCACTTACAC-CAAGTGTGGTTGCGGGCCTTGG-TTGACACCCAGAT	2160
Query	2161	GCATGGTCGACTACCCGTAATAGGCTTTGGCACTATCCTTGTACCATCAA-TTACACCATA	2219
Sbjct	2161	GCTTGGTCCACTACCCATACAGGCTTTGGCACTACCCCTGCATGTCAACTT-TACCATC	2219
Query	2220	TTCAAAGTCAGGATGTACGTGGGAGG-GTCGAGCACAGGCTGGAAGCGGCCTGCAACTG	2278
Sbjct	2220	TTCAAGGTTAGGATGTACGTGGG-GGGAGTGGAGCACAGGCTCGAAGCCGATGCAATTG	2278

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Query	2339	GCTGTCCACCACACAGTGGCAGGTCCCTT-CCGTGTTCTTTACAGACCTGCGAGCCT-TG	2396
Sbjct	2339	GCTGTCTACAAACGAGGTGGCAGGT-ATTGCCCTGTTCCTTACCACCCCTACC-GGCTCTG	2396
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Sbjct	2397	TCACCTGCTTTGATCCATCTCCATCAGAACGTCGTGGACGTACAATACCTGTACGCTATA	2456
Query	2457	GGGTCAAGC-ATCG-CGTCTGGGCCATTAAGTGGGAGTACGTCGT-TCTCCTGTTCCTT	2513
Sbjct	2457	GGGTC-GGCGGTTGTC-TCTTTGCAATCAAAATGGGAGTATGTCCTGT-TGCTCTTCCTT	2513
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Query	2573	GGAGGCGGCTTTGGAGAACCTCGTAATCTCAATGACAGCATCCCTGGCCGGGACGACGG	2632
Sbjct	2573	TGAGGCGGCGCTTAGAGAACCTGGTGGTCTCAACGCGGCATCCGTGGCCGGGGCGCATGG	2632
Query	2633	TC-TTGTGTCCTTCCCTCGTGTCTTCTGCT-TTGCCTGGTATC-TGAAGGGTAGG-TGGG	2688
Sbjct	2633	-CATTCTCTCTCTCTCGTGTCTTCTGCT-TGCTGCCTGGTA-CATCAAGGCGAGGCT-GG	2688
Query	2689	TGCCC-GGAGCGGTC-TACGCCCTCTACGG-GATGTGGCCTCTCCTCTGCTCTCTGCTGG	2745
Sbjct	2689	T-CCCTGGGGCGG-CATATGCCCTCTACGGCG-TATGGCGCTACTCTGCTCTCTGCTGG	2745
Query	2746	CGTTGCC-TACGGCGGCATACG-CACTGGACAC-GGAGGTGGCCGCGCTGCTGGCGGGG	2802
Sbjct	2746	CGTTACCACCA-CGAGCATACGCCA-TGGAC-CGGGAGATGGCAGCATCTGTCGGGAGGG	2802
Query	2803	TTGTTCTT-TGCGGGT-TAATGGCGC-TGA-CTCTGTCGCATATTACAAGC-GCTAT-A	2856
Sbjct	2803	CGGTT-TTCGT-AGGTCTGAT-ACTCTTGACCT-TGTCACCGCCTATAAGCTG-T-TCC	2856
Query	2857	TCAGCT-GG-TGCAATGTGGTGGCTT-CAGTATTTTCTGACCAGAGTAGAAGCGCA-AC-T	2911
Sbjct	2857	TC-GCTAGGCT-CATATGGTGG-TTACAATATTTATCACCAGGGCGG-AG-GCACACTT	2911
Query	2912	GCACGTGTGGGTTTCAACGCTCCCGGGGGCGCGATGCCGTCATCTTACTCAT	2971
Sbjct	2912	GCAAGTGTGGATCCCCCCCCCAACGTTCCGGGGGGCGCGATGCCGTCATCTTACTCAC	2971
Query	2972	GTGTGTAG-TACACC-GACCCTGGTATTGA-CATCACCAAATAC-TCTGGGCAT-C	3026
Sbjct	2972	GTGCG-CGATCCACCAGA-GCTAATCTT-ACCATCACCAAAAT-CTTGTCTGCCATAC	3027
Query	3027	TTCCGACCCCT-TTGGATTCTTCAAGCCAGT-TTGCTTAAAGTCCCTACTTCTGTCGCG	3084
Sbjct	3028	-TCGGTCCACTCATAG-TGCTCCAGGCTGGTATAAC-CAAAGTCCGCTACTTCTGTCGCG	3084
Query	3085	TTCAAGGCCCTT-CGCCGAT-C-TGCGCGCTAGCGCGGAAGATAGCCGGAGGTCATTACG	3141
Sbjct	3085	CACACGGGC-TCATTG-G-TGCATGCATGCTGGTGGGAGGTTGCTGGGGGTCATTATG	3141
Query	3142	TGCAAAATGGC-CATCATCAAGTTAGG-GGCGCTTACTGGCACCTATGTGTATAACACTT	3199
Sbjct	3142	TCCAAATGGCTC-TCATGAAGTT-GGCCGCACTGACAGGTACGTACGTTTATGACACTT	3199
Query	3200	CACCCCTCTTCGAGACTGGCGCACAAAC-GGCGCTGCGAGATCTGGCCGTGGCTTGGAAAC	3258
Sbjct	3200	CACCCCATTCGCGGACTGGGCCAC-GCGGGCTTACGAGACTTTCGGTGGCAGTTGAGC	3258
Query	3259	CAGTCGTCTTCTCCCGA-ATGGAGACCAAGCTCATCAGCTGGGGGGCAGATACGCCCGG	3317
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Query	3318	TGCGGTGACATCATCAACGGCTTGGCCGCTCTCTGCCGTAGGGGCCA-GGAGATAC-TGC	3375
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Query 3376 TTGGG-CCAGCCGAC-GGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCATCACGGC 3433
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Sbjct 3376 -TGGGACCCGACACAGCCTTGAAGGGC-AGGGGTGGCGACTCTCGCGCTATTACGGC 3433
Query 3434 GTACGCCAGCAGACGAGAGGCCCTCCTAGGGTGTATAATCACCAGCCTGACTGGCGCGGA 3493
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Sbjct 3434 CTACTCCCAACAGACGCGAGGCCCTACTTGGCTGCATCATCACTAGCCTACAGGCCGCGGA 3493
Query 3494 CAAAAACCAAGTGGAGGGTGAGGTCC-AGATCGTGTCAACTGTACCCAAACCTTCTCTGG 3552
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Sbjct 3494 CAGGAACAGGTCGAGGGGGAGGTCCAAAG-TGGTCTCCACCGCAACAACAATCTTCTCTGG 3552
Query 3553 CAACGTGCATCAATGGGGTATGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCATCG 3612
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Sbjct 3553 CGACCTGCGTCAATGGCGTGTGTGGACTGTCTATCATGTGCGCGCTCAAAGACCCCTTG 3612
Query 3613 -CATCACCAAGGGTCTGTCTATCCAGATGTATACCAATGTGGACAAGACCTTGTGGGC 3671
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Sbjct 3613 CCGGC-CCAAAGGGCCCAATACCCAAATGTACCAATGTGGACCAGGACCTCGTGGC 3671
Query 3672 TGGCCCGCTCCTCAAGGTTCCCGCTCATGTACACCCGTGACCTGCGGCTCCTCGGACCTT 3731
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Sbjct 3672 TGGCAAGCGCCCCCGGGGCGCGTTCCTTGACACCATGCACTGCGGAGCTCGGACCTT 3731
Query 3732 TACCTGGTACAGAGGCACGCCGATGTCTATCCCGTGC CGCGCGAGGTGATAGCAGGGGT 3791
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Sbjct 3732 TACTTGGTACAGAGGCATGCCGATGTCTATCCCGTGC CGCGCGGGGGCGACAGCAGGGGG 3791
Query 3792 AGCCTGCTTTCGCCCC-GGCCCATTTCTACTTGAAGGCTCCTCGGGGGTCCGCTGTT 3850
      |||
Sbjct 3792 AGCCCTACTCTC-CCCCAGGCCGCTCTCTACTTGAAGGCTCTTCGGGCGGTCCACTGCT 3850
Query 3851 GTGCCCGCGGGACAGCCGTGGG--CTATTACGGGCGCGGTGTGCACCCGTGGAGTG 3908
      |||
Sbjct 3851 CTGCCCTCGGGGACAGCTGTGGGCACTT-TTC-GGGCTGCCGTGTGCACCCGAGGGGT 3908
Query 3909 GCTAAAGCGGTGGACTTTAT-CCCTGTGGAGAACCTA-GG-GACAACCATGAGATCCCCG 3965
      |||
Sbjct 3909 GCGAAGGCGGTGGACTTTGTACCC-GTCGAG--TCTATGAAACCACTATGCGGTCCCCG 3965
Query 3966 GTGTTACCGGACAACCTCTCTCCACCAGCAGTGC CCGGAGAGC-TTCCAGGTGGCCACCT 4024
      |||
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Query 4025 GCATGCTCCC-ACCGCAGCGGTAAAGACCAAGGTC CCGGTGCTGCTACGAGCCC-AG 4082
      |||
Sbjct 4025 ACACGC-CCCTACTGTAGCGGCAAGAGCACTAAGGTGCCGGCTGCTATGAGCCCAAG 4083
Query 4083 GGTACAAAGGTG-TGGTGCTCAACCCCTCTGTGTGCTGAACGCTGGGCTTT-GGTGCTT 4140
      |||
Sbjct 4084 GG-TATAAGGTGCTT-GTCTGAACCGTCCGTGCGCGCACCCCTAGG-TTTCGGGGCGT 4140
Query 4141 ACATGTCCAAGGCCCATGGGGTTGATCCTAATATCAGGACCGGGGTGAGAACATTACCA 4200
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Sbjct 4141 ATATGTCTAAGGCACATGATATCGACCTTAACATCAGAACCGGGGTAAAGGACCATACCA 4200
Query 4201 CTGGCAG-CCCCATCAGTACTCCACCTACGGCAAGTTCCTTGGCGACGGGGGTGCTCA 4259
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Sbjct 4318 TCTTGGGCATCGCACTGTCTTGTGACCAAGCGGAGACGGGTGGAGCGGACTCGTGTGC 4377
Query 4378 TCGCCACTGTACCCCTCCGGGCTCCGTCACTGTGTCC-CATCCTAACATCAGGAGGTT 4436
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Sbjct 4378 TCGCCACCGCTACGCTCCGGGATCGGTACCGTG-CCACATCCAACATCAGGAGGTT 4436
Query 4437 GCTCTGTCCACCACGGAGAGATCCCTTTTACGGCAAGGCTATCCCCCTCGAGGTGATC 4496
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Sbjct 4437 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCCATCGAGACCATC 4496

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Query	4497	AAGGGGGGAAGACATCTCATCTTCTGCCACTCAAAGAAGAAGTGCAGAGCTCGCCGG	4556
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Query	4557	AAGCTGGT-C-GCAATGGGCATCAATGCCGTGGCTACTACCGCGTCTTGACGTGCTG	4614
Sbjct	4557	AAGCT-GTCCGGGCTCGGAC-TCAATGCTGTAGCATATTACCGGGGCTTGATGATCCG	4614
Query	4615	TCATCCCGACCACGCGCATGTTGTCGTCGT-GTCGACCGATGCTCTCATGACTGCGCTT	4673
Sbjct	4615	TCATACCAACTAGCGGAGACGTCATTGTGCTAG-CAACGCGACGCTCTAATGACGGGCTT	4673
Query	4674	ACCGCGGACTTCGACTCTGTGATAGACTGCAACACGTGTGCTACTCAGACAGTCGATTT	4733
Sbjct	4674	ACCGCGGATTCGACTCAGTGATGACTGCAATACATGTGTACCCAGACAGTCGACTTC	4733
Query	4734	AGCCTTGACCTACCTTTACCAATTGAGACAACCA-CGCTCCCCAGGATGCTGTCTCCA-	4791
Sbjct	4734	AGCCTGGACCCGACCTTACCATTGAGACGACGACCG-TGCCACAAGACGGGTGT-CAC	4791
Query	4792	GGACTCAACGCCGGGGCAGGACTGGCAGGGGGAAGCAGGCATCTATAGATTTTGGGCAC	4851
Sbjct	4792	GCTCGCAGCGGCGAGGACGAGCTGGTAGGGGAGGATGGGCATTACAGGTTTGTGACTC	4851
Query	4852	CGGGGAGCGCCCTCCGGCATGTTGCACTCGTCCGTCCTCTGTGAGTGCTATGACGCGG	4911
Sbjct	4852	CAGGAGAACGGCCCTCGGGCATGTTGATTCTCGGTTCTGTGCGAGTGCTATGACGCGG	4911
Query	4912	GCTGTGCTTGGTATGAGCTCACGCCCGCCGAGAC-TACAGTTAGGCTACGAGCGTACATG	4970
Sbjct	4912	GCTGTGCTTGGTACGAGTCTACGCCCGCCGAGACCT-CAGTTAGGTTGCGGGCTTACCTA	4970
Query	4971	AACACCCCGGGGCTT-CCGTTGTGCCAGGACCATTTGAATTTTGGGAGGGCGTCTTTAC	5029
Sbjct	4971	AACACACCAAGG-TTCCCGCTGTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTAC	5029
Query	5030	GGGCTCACTCATATAGATGCCACTTT-TTATCCAGACAAGCAGAGTGGG-GAGAAC	5087
Sbjct	5030	AGGCCCTACCCACATAGACGCCA-TTCTGTGCCAGACTAAGCAG-GCAGGAGACAAC	5087
Query	5088	TTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCTAGGGCTCAAGCCCCCCCCA	5147
Sbjct	5088	TTCCCCCTACCTGGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTCCA	5147
Query	5148	TCGTGGGACAGATGTGGAAGTGTGTTGATCCGCCCTTAAACCC-ACCCCTTACGGGCAAC	5206
Sbjct	5148	TCGTGGGACCAATGTGGAAGTGTCTCATACGGCT-AAAGCCTACGCTGCACGGGCAAC	5206
Query	5207	ACCCCTGCTATACAGACTGGGCGCTGTTGAGAATGAAGTCAC--CCTGACGCACCAATC	5264
Sbjct	5207	GGCCCTGCTGTATAGGCTGGGAGCCGTTCAAACAGAGGTACTACC--ACACACCCATA	5264
Query	5265	ACCAAAATACATCATGACATGCATGTCGGCCGACCTGGAGGTGCTCACGAGCACTGGGTG	5324
Sbjct	5265	ACCAAAATACATCATGCGATGCATGTCGGCTGACCTGGAGGTGCTCACGAGCACTGGGTG	5324
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Sbjct	5325	CTGGTAGGCGGAGTCTTAGCAGCTCTGGCCGCGTATTGCGCTGACAAACAGGACGCGTGGTC	5384
Query	5385	ATAGTGGGACAGATCGTCTTGTCCGGGAAGCGGCAATATACCTGACAGGAGGTTCTC	5444
Sbjct	5385	ATTGTGGGACAGATCATCTTGTCCGGAAAGCGGCGCATCATCCCGACAGGGAAGTCCCT	5444
Query	5445	TACCAGGAGTTTCGATGAGATGGAAGAGTGCTC-TCAGCACTTACCGTACATCGAGCAAGG	5503
Sbjct	5445	TACCGGAGTTTCGATGAGATGGAAGAGTGCGCTCA-CACCTCCCTTACATCGAACA-GG	5502
Query	5504	GA-TG-ATGCTCGCTGAGCAGTTCAAGCAGAAGGCCCTCGGCCCTCTGCAGACCGCTCC	5561
Sbjct	5503	GAATGCA-GCTCGCGGAACAATTCAAACAGAAGGCAATCGGGTGTGTCGAACACGCCACC	5561
Query	5562	C-GCCATGCAGAGGTTA-T-CACCCCTGCTGTCCAGACCACTGGCAGAACTCGAGGTC	5618
Sbjct	5562	AAGCAA-GCGGAGGCTGCTGCTCCCGTGGTGA-AT-CCAAGTGGCGGACCTCGAAGCC	5618

Query	5619	TTTTGGGCGAAGCACAATGTGGAATTTTCATCAGTGGGATACAATACTTGGCGGGCCTGTCA	5678
Sbjct	5619	TTCGCGGCGAAGCATATGTGGAATTTTCATCAGCGGGATACAATAATTTAGCAGGCTGTGTC	5678
Query	5679	ACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGC-TGCCGTACCCAG	5737
Sbjct	5679	ACTCTGCCTGGCAACCCCGCATAGCATCACTGATGGCAATTCACAGCCT-CTATCACCAG	5737
Query	5738	CCCACTAACCACCTGGCCAAACCTCCTCTTCAACATATTgggggggTGGGTGGCTGCCCA	5797
Sbjct	5738	CCCGCTACCAACCCCAACATACCTCCTGTTTAAACATCCTGGGGGGATGGGTGGCCGCCCA	5797
Query	5798	GCTCGCCGCC-CCCGGTGCCGCTACTGCTTTT-GTGGTGCTGGCTAGCTGGCGCCGCC	5855
Sbjct	5798	ACTTGCT-CCTCCAGCGCTGCTTCTGC-TTTCGTAGCGCCGGCATCGCTGGAGCGCT	5855
Query	5856	ATCGGCAGCGTGGCATGGGGAAGGTCTCGTGGACATTTCTG-CAGGGTATGGCGC-GG	5913
Sbjct	5856	GTTGCGCAGCATAGGCTTGGGAAGGTGCTTTGGATATT-TTGGCAGGTTATGGAGCAGG	5914
Query	5914	CGGTGGCGGGAGCTCTTGTAGCATTTCAAGATCATGAGCGGTGAGGTCCCTTCACGGAGG	5973
Sbjct	5915	G-GTGGCAGGCGCGCTCTGTGCCCTTAAAGGTATGAGCGCGAGATGCCCTTCACCGAGG	5973
Query	5974	ACCTGGTCAAICTGCTGCC-GCCATCCTCTCGCTGGAGCCCTTGTAGTCGGTGTGGTC	6032
Sbjct	5974	ACCTGGTTAACTTACT-CCCTGCTATCCTCTCCCTTGGCGCCTAGTCGTGGGGTCTGTG	6032
Query	6033	TGCGCAGCAATACTGCGCCGGCAGTTGGCCC-GGGCGAGGGGGCAGTGCAATGGATGAA	6091
Sbjct	6033	TGCGCAGCGATACCTGCGCTCGCACGTGGGCCCAGGG-GAGGGGGCTGTGCAAGTGATGAA	6091
Query	6092	CCGGCTAATAGCCTTCGCTCCCGGGGGAACCATGTTTCCCGCAGCACTACGTGCCGGA	6151
Sbjct	6092	CCGGCTGATAGCGTTTCGCTTCGCGGGGTAAACACGCTCTCCCGCAGCACTATGTGCTGA	6151
Query	6152	GAGCGATGACAGCGCCCGCGTCACTGCC-ATACTCAGC-AGCCTCACTGTAACCCAGCTC	6209
Sbjct	6152	GAGCGACGCTGACGACAGTGTCACT-CAGATCCTCT-CTAGTCTTACCATCACTAGCTG	6209
Query	6210	CTGAGGCGCATGTCATCAGTGGAT-AAGCTCGGAGTG-TACCACTCCATGCTCCGGTTCTCT	6267
Sbjct	6210	CTGAAGAGGCTTCACCACTGGATCAA-CGAGGACTGCT-CCAGCCATGCTCCGGCTCGT	6267
Query	6268	GGCTAAGGGACATCTGGGACTGGATATGCGA-GGTGCTGAGC-GACTTT-AAGACCTGGC	6324
Sbjct	6268	GGCTAAGAGATGTTTGGGATGGATATGC-ACGGTGTTGA-CTGA-TTTCAGACCTGGC	6324
Query	6325	TGAAAG-CCAAGCTCATGCCACAACCTGCTGGGATTCCCTTTGTGTG-C-TGCCAGCGCG	6381
Sbjct	6325	TCCA-GTCCAAGCTCCTGCCCGATTGCC-GGGAGTCCCTTCT-TCTCATGTCAACGTG	6381
Query	6382	GGTATAGGGGGGCTGGCGAGGAGACGGCATTATGCACACTCGC-TGCC-ACTGTGGAGC	6439
Sbjct	6382	GGTACAGGGGAGTCTGGCGGGGCGACGGCATATGCAAAAC-CACCTGCCCA-TGTGGAGC	6439
Query	6440	TGAGATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCTAGGACCTGCAG	6499
Sbjct	6440	ACAGATACCGGACATGTGAAAAACGGTTCATGAGGATCGTGGGGCTAGGACCTGTAG	6499
Query	6500	GAACATGTGG-AGTGGGACGTTCCCATTAACGCTACACGAGGGCCCTGTACTCCCC	6558
Sbjct	6500	TAACACGTGGCA-TGGAACATTTCCCATTAACGCTACACGAGGGCCCTGTACGCCCC	6557
Query	6559	TTCTGT-GCGCGAACTATAAGTTCG-CGCTGTGGAGGGTGTCTGCAGAGGAATACGTGGA	6616
Sbjct	6558	TCCCGGCGGCCAAATTATTC-TAGGGCGCTGTGGCGGGTGGCTGTGAGGAGTACGTGGA	6616
Query	6617	GATAAGCGGGTGGGGGACTTCCACTACGT-ATCGGGTATGACTACTGACAATCTTAAA-	6674
Sbjct	6617	GGTTACGCGGGTGGGGGATTCCACTACGTGA-CGGGCATGACCACTGACAA-CGTAAG	6674
Query	6675	TGCCCGTGCCAGATCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCCTACAC	6734
Sbjct	6675	TGCCCGTGTACAGTTCCGGCCCCGAATCTTTCACAGAAGTGAATGGGGTGCCTGTGAC	6734

Query	6735	AGGTTTGGGCCCCCTTGC AAGCCCTTCTCGGGGAGGAGGT-ATCATTCA-CAGTAGGAC	6792
Sbjct	6735	AGGTACGCTCCAGCGTGCAAAACCCCTCTACGGGAGGAGGTCA-CATTCTGT-GTCGGGC	6792
Query	6793	TCCA-CGAGTACCCGGTGGGGTCGAAATTACCTTGCAGAGCCGAACCGGACGTAGCCGTG	6851
Sbjct	6793	TCAATCAA-TACCTGGTTGGGTACAGCTCCCATGCGAGCCGAACCGGACGTAGCAGTG	6851
Query	6852	TTGACGTCCATGCTCACTGATCCCTCCCATATAACAGCAGAGGCGCGCGGGAGAAGGTTG	6911
Sbjct	6852	CTCACTTCCATGTCTACCGACCCCTCCCAATTACGGCGGAGAGCGCTAAGCGTAGGCTG	6911
Query	6912	GCGAGAGGG-TCACCCCTTC-TATGGCCAGCTCTCGGTAGCCAGCTGTCCGCTCCAT	6969
Sbjct	6912	GCCAG-GGGATCTCCCCCTCTCT-TGGCCAGCTCATCAGCTAGCCAGCTGTCTCGCCCTT	6969
Query	6970	CTCTC- AAGGCAACTTGACCGGCCAACATGACTCCCTGACCGCAGCTCATAGAGGCT	7028
Sbjct	6970	C-CITGAAGGCAACATGCACTACCCTGTCATGACTCCCGGAGCGTGACCTCATCGAGGC	7028
Query	7029	AACCTCTGTGGAGGCAAGAGATGGGCGGAACATCACCAGGGTTGAGTCAGAGAAACAA	7088
Sbjct	7029	AACCTCTGTGGCGGCAAGAGATGGGCGGAACATCACC CGCTGGAGTCAGAAAAAAG	7088
Query	7089	GTGGTGATTCTGGACTCCTTCGATCCGCTTGTGGCAGAGGAGGATGAGCGGGAGGTCTCC	7148
Sbjct	7089	GTAGTAATTTTGGACTCTTTCGAGCCGCTCCAAGCGGAGGAGGATGAGAGGGAAGTATCC	7148
Query	7149	GTACCTGCAGAAATTTCTCGGGAAGTCT-GGAGATTGCC-CGGCCCTTCCCCCTCTGGG	7206
Sbjct	7149	GTTCGGCGGGAGATCTCTCGGAGGTC-CAGGAAATTC-CCTCGAGCGATGCCCATATGGG	7206
Query	7207	GCGGGCCGGACTACAACCCCGCTAGT-AGAGACGTGGAAAAAGCCTGACTACGAACCA	7265
Sbjct	7207	CACGCCCGGATTACAACCTCCACT-GTTAGAGTCTCTGGAAGGACCCGGACTAGTCCTCT	7265
Query	7266	CCTGTGGTCCATGCTGCCCGCTACCACT-CCACGGTCCCTCCTG-TGCTCCGCCTC	7323
Sbjct	7266	CCAGTGGTACAGGGGTGTCATTGCCCGCTGCCAAGG-CCCTCC-GATACCACTCCAC	7323
Query	7324	GGAAAAAGCGTACGGTGGTCCACCGAATCAACCTATCTACTGCTTTGGCCGAGCTTG	7383
Sbjct	7324	GAGGAGAAAGGACGGTGTGCTCTTGCAAACTACCGTGCTCTCGGCTGCACCGAGCTCG	7383
Query	7384	CCACAGAA-AGTTTGGCAGCTTCTCAA-CTTCCGGATTT-ACGGCTGACCAATGACGA	7439
Sbjct	7384	CCAC-AAAGACCTTTCGCGAGCTTCG-AATCGTC-GGCCGTGCAGAG-CGGCA---CGGCA	7436
Query	7440	ACATCTCTGA-GCCC-GCCCTTCTG--G-CTG-----G-ACTCCGACGTTGAGTCC	7493
Sbjct	7437	ACGGCTCTCTTGACAGCCC-TCC-GACGACGGCGACGGGGA-TCCGACGTTGAGTGC	7493
Query	7494	TATTCTTCATG-----TGGAGGGGAGCCTGGGGATCCGGATCTCAGCGCAGGGTCA	7553
Sbjct	7494	TACTCTTCATGCCCCCTTGGAGGGGAGCGGGGGATCCCGATCTCAGCGCAGGGTCT	7553
Query	7554	TGGTCAGCGGTCACTAGTGG-GCCGCAACGGAAGATGCTGTGTGCTGCTCAATGCTTA	7612
Sbjct	7554	TGGTCTACCGTAAGC-GAGGAGGCT-AGT-G-AGGACGTCGTGCTGCTCGATGCTTA	7609
Query	7613	TTCTTGACAGGCGCACTCG-TCACCCCGTGCGCTGCGGAGAA-CAAAAACCTGCCATC	7670
Sbjct	7610	CACATGCAAGCGCCCT-GATCAGCCATGCGCTGCGGAGGAAACCAAG-CTGCCATC	7667
Query	7671	AACGCACTGAGCAACTCGTTGCTACGCCATCAAAATCT-GGTGTAATCCACCACTTCAAG	7729
Sbjct	7668	AATGCACTGAGCAACTCTTTGCTCCGTACCAACAA-CTTGCTATGTACTACAACATCTCG	7726
Query	7730	CAGTGTCTGCCAAAGGCAGAAAGATCACATTTGACAGACTGCAAGTTCTGGAC-AGCC	7785
Sbjct	7727	CACGCAAGGCTCGGCCAGAAAGAGTGACCTTTGACAGACTCGAGGCTCTGGACGA-CC	7785
Query	7789	ATTACAGGACGTCTCAAGGAGTCAAAG-AGCGGCTCAAAAGTGAAGGCTAA-CTT	7846
Sbjct	7786	ACTACCGGAGCTGCTCAAGGAGATGAAGGCGAA-GGCGTCCACAGTTAAGGCTAAACTT	7844

Query	7847	GCTATCCGTAGAGGAAGCTTGCA-GCCTGACGCCCCACATTACGCAAAATCCAAGTTTG	7905
Sbjct	7845	-CTATCCGTGGAGGAAGCCTGTAAGC-TGACGCCCCACATTGCGCCAGATCTAAATTTG	7902
Query	7906	GCTATGGGGCAAAAGACGTCGCTTGCC-ATGCCAGAAAGGCCGT-AGCCCACTCAACTC	7963
Sbjct	7903	GCTATGGGGCAAAAGGACGTCGGAACCTAT-CCAGCAAGGCCGTAAACC-ACATCCGCTC	7960
Query	7964	CGTGTTGAAAAGACCTT-CTGGAAGACAGTGTA-ACACCAATAGACACTACCATCATGGCC	8021
Sbjct	7961	CGTGTTGGAAGGAC-TTGCTGGAAGACACTG-AGACACCAATTGACACCACCATCATGGCA	8018
Query	8022	AAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGTTCGTAAGCCAGCTCGTCTCATC	8081
Sbjct	8019	AAAAATGAGGTTTTCTGCGTCCAACAGAGAAGGGGGCGCAGCCAGCTCGCCCTATC	8078
Query	8082	GTGTTCCCCGACCTGGGCGTGCGCGTGTGCGAGAAGATGCCCTGTACGACGTGGT-TAG	8140
Sbjct	8079	GTATTCACGAGATTGGGGTTCGTGTGTGCGAGAAATGCCCTTTACGATGTGGTCTC-	8137
Query	8141	CAAGCTCCCCCTGGCGGTGATGGGAAGCTCC-TACGGATTCCAATACTCACCAGGACAGC	8199
Sbjct	8138	CACCTCCCTCAGGCGGTGATGGGCT-CTTCATACGGATTCCAATACTCTCCTGGACAGC	8196
Query	8200	GGGTGAATTCCTCGTGCAA-GCGTGGAA-GTCCAAGAAGAC-CCCGATGGGGTTCTCGT	8256
Sbjct	8197	GGGTGAGTTCCTGGTG-AATGCCTGGAAAG-CGAAGAA-ATGCCCTATGGGCTTCGCAT	8253
Query	8257	ATGATACCCGCTGTTTTGACTCCACAGTCACTGAGAGCGACATCCGTACGAGGAGGCAA	8316
Sbjct	8254	ATGACACCCGCTGTTTTGACTCAACGCTCACTGAGAATTGACATCCGTGTTGAGGAGTCAA	8313
Query	8317	TTTACCAATGTTGTGACTGGACCCCG-AAGCCCG-CGTGGCCATCAAG-TCCCTCACTG	8373
Sbjct	8314	TCTACCAATGTTGTGACTTGG-CCCCGAAGCCAGACA-GGCCAT-AAGGTGCTCACAG	8370
Query	8374	AGAGGCTTTAIGTTGGGGCCCTCTTACCAATTC-AGGGGGGAAAATGCGGCTACCGC	8432
Sbjct	8371	AGCGGCTTTACATCGGGGGCCCTGACTAATTTCTAAGGGC-AGAACTGCGGCTATCGC	8429
Query	8433	AGGTGCCGCGCAGCGCGGTACTGACAACTAGCTGTGGTAACACCTCAGTGTGTATC	8492
Sbjct	8430	CGGTGCCGCGCAGCGGGTACTGACGACCACTGCGGTAAATACCTCACATGTTACTTG	8489
Query	8493	AAGGCC-CGGGACGCTGTGAGCCGC-AGGGCTCCAGGACTGCACCATGCTCGTGTGTG	8550
Sbjct	8490	AAGGCCGCTG-CGGCTGTGAGCTGCGAAG-CTCCAGGACTGCACGATGCTCGTATGCG	8547
Query	8551	GCGAGCAC-TTAGTCGTTATCTGTGAAAGTGCAGGGGGTCCAGGAGGACGCGGCGAGCCTG	8609
Sbjct	8548	GAGAGGACCTT-GTCGTTATCTGTGAAAGCGCGGGGACCCAAGAGGACGAGGCGAGCCT-	8605
Query	8610	A-GAGCCTTCACGGAGGCTATGACCAGGTACTCCG	8667
Sbjct	8606	ACGGGCCTTCACGGAGGCTATGACTAGATACTCTGCC	8664
Query	8668	CAGAATACGACTTGGAGCTT-ATAACATCATGCTCCTCCAAACGTGTCAGTGCGCCACGAC	8726
Sbjct	8665	CAGAATACGACTTGGAG-TTGATAACATCATGCTCCTCCAAATGTGTCAGTGCAGCAGAT	8723
Query	8727	GGCG-CTGG-AAAGAGGGTCTACTACCTTACCCTGACCTTACAACCCCCCTCGGAGAG	8784
Sbjct	8724	G-CATCTGGCAAA-AGGGTGTACTATCTACCCGTGACCCCAACCCCCCTTGGCGGG	8781
Query	8785	CCGCGTGGGAGACAGCAAGACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGT	8844
Sbjct	8782	CTGCGTGGGAGACAGCTAGACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGT	8841
Query	8845	TTGCCCCCACT-GTGGCGAGGATGATACTGATGACCAATTTCTT-TAGCGTCTT-CA	8901
Sbjct	8842	ATGCGCCAC-CTTGTTGGCAAGGATGATCCTGATGACTCAATTTCTTCTC-CATCCTT-	8898
Query	8902	TAGC-CAGGGATCAGCTTGAACAGGCTCTTA-ACGTGTGAGATCTACGGAGCCTGCTACTC	8959
Sbjct	8899	TAGCTCAGGAA-CAACTTGAAAAGCCCT-AGATTGTGAGATCTACGGGGCTGTTACTC	8956

Query	8960	CATAGAACCACTGGATCTACCTCCA-ATCATTCAAAGACTCCATGGCCCTACGGCGATTTT	9018
Sbjct	8957	CATTGAGCCACTTGACCTACCCTC-AGATCATTTCAAGACTCCATGGCCCTTAGCGCATTTT	9015
Query	9019	CACTCCACAGTTACTCTCCAGGTGAATCAATAGGGTGGCCGATGCCCTCAGAAAACTTG	9078
Sbjct	9016	CACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTTCATGCCCTCAGGAAACTTG	9075
Query	9079	GGGTCCC GCCCTTGCGAG-CTTGGAGACACCGGGGCCGGAGCGTCCGCCTAGGCTTCTG	9137
Sbjct	9076	GGGTACCGCCCTTGCAGAGTCT-GGAGACATCGGGCCAGAAGTGTCCGCCTAGGCTACTG	9134
Query	9138	TCC-AGAGGAGGCGAGGGCTGCCA-TATGTGGCACTACTCTTCACTGGGCAGTAAGAA	9195
Sbjct	9135	TCCGAGGGGGG-AGSGCTGCCACT-TGTGGCACTACTCTTCACTGGGCAGTAAGAA	9192
Query	9196	CAAGCTCAAACCTACTCCAATAGCGGCTGCGCCG-CTGGAATCTTGGCGGTGGTTC	9254
Sbjct	9193	CCAAGCTCAAACCTACTCCAATCCCGGCTGC-GTCCAGTTGGATTATCAGCTGGTTC	9251
Query	9255	ACGGCTGGCTACAGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGCCCCCGTGG	9314
Sbjct	9252	GTTGCTGGTTACAGCGGGGGAGACATATATCACAGCGTGTCTCGTGCCGACCCCCGTGG	9311
Query	9315	TTC-TGGTTTTGGCTACTCCTGCTCGTGCAGGGGTAGGCATCTACCTCCTCCCAACCG	9373
Sbjct	9312	TTCATG-TGGTGCTACTCCTACTTTCTGTAGSGGTAGGCATCTACTACTCCCAACCG	9370
Query	9374	ATGAAGGTTGGG-G-TAAACACTTC-GGCCCTCTTAAGCCATTTCCTGTTTTT---TTT	9427
Sbjct	9371	ATGAAGC--GGGAGCTAAACACTCCAGGCCAAT-AGGCCAT--CCTGTTTTTTTCCCTTT	9425
Query	9428	ttttttttt-tttttttttttccttttttttttttttttttttttttcct-tc-tttttttt-gct-	9481
Sbjct	9426	TTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCCTTTTTTTTCTCTC	9485
Query	9482	tctttttttccctt-ctttAAT--GGTGGCTCCATCTTAGCCCTTAGTACCGCTAGCTGTG	9538
Sbjct	9486	TT-TTTTCTTTTCTTCTTCTTGTGGCTCCATCTTAGCCCTTAGTACCGCTAGCTGTG	9544
Query	9539	TAAGGTCCGCTGAGCCGCTACTGTCAGAGAGTGCTGATACTGGCCCTCTTCGCAGATCA	9596
Sbjct	9545	AAGGTCCGCTGAGCCGCTTGACTGCAGAGAGTGCTGATACTGGCCCTCTTCGCAGATCA	9602

Score = 3354 bits (1816), Expect = 0.0
Identities = 3942/4944 (79%), Gaps = 244/4944 (4%)
Strand=Plus/Plus

Query	1	GCCAGCCCTCTGA-TGGGGGCGACATCCACCATGA-ATCACTCCCCTGTGAGGAAGTAC	58
Sbjct	1	GCCAGCCCCC-GATTGGGGCGCACTCCACCAT-AGATCACTCCCCTGTGAGGAAGTAC	58
Query	59	TGCTTTCACGCAGAAAGCGCTAGCCATGGCGTTAGTATGAGTGTCTGTGAGCCTCCAGG	118
Sbjct	59	TGCTTTCACGCAGAAAGCGCTAGCCATGGCGTTAGTATGAGTGTCTGTGAGCCTCCAGG	118
Query	119	AcacccccTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCC	178
Sbjct	119	ACCCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCC	178
Query	179	AGGACGACCGGGTCTCTTCTTGGATAAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCC	238
Sbjct	179	AGGACGACCGGGTCTCTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCC	238
Query	239	CCGCAAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAGGCCCTTGTGGTACTGCCTGATA	298
Sbjct	239	CCGCGAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAGGCCCTTGTGGTACTGCCTGATA	298
Query	299	GGGTGCTTCGAGTGGCCCGGGAGGTCTCTGATGACCGTGCACATGAGCAGCAATCTTAA	358
Sbjct	299	GGGTGCTTCGAGTGGCCCGGGAGGTCTCTGATGACCGTGCACATGAGCAGCAATCTTAA	358
Query	359	ACCTCAAAGAAAAACCAACGTAACACCAACCGTCGCCACAGGACGTCAAGTTCCTCGGG	418
Sbjct	359	ACCTCAAAGAAAAACCAACGTAACACCAACCGTCGCCACAGGACGTCAAGTTCCTCGGG	418

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Query 419      TGGCGGTGATGATCGTTGGTGGAGTTTACTTGTGCGCGCAGGGGCCCTAGATTGGGTGT 478
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Sbjct 419      CGGTGGTCAGATCGTCGGTGGAGTTTACCTGTGCGCGCAGGGGCCCCAGGTTGGGTGT 478
                |||
Query 479      GCGCGCGACGAGGAAAGACTTCCGAGCGGTGCGAACCTCGAGGTAGACGTCAGCCTATCCC 538
                |||
Sbjct 479      GCGCGCGACTAGGAAAGACTTCCGAGCGGTGCGAACCTCGTGAAGGCGACAACTATCCC 538
                |||
Query 539      CAAGGCACGTCGCGCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCCTTGGCCCTCTA 598
                |||
Sbjct 539      CAAGGCTCGCCAGCGCCGAGGGTAGGGCTTGGGCTCAGCCCGGGTACCCCTTGGCCCTCTA 598
                |||
Query 599      TGGCAATGAGGG-TTGGCGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTCTCGGCCTA 657
                |||
Sbjct 599      TGGCAATGAGGGCTTG-GGGTGGCAGGATGGCTCCTGTCAACCCGTGGCTCTCGGCCTA 657
                |||
Query 658      GCTGGGGCCCAAGACACCCCGGCGTAGGTGCGCAATTGGGTAAAGGTATCGATACCC 717
                |||
Sbjct 658      GTTGGGGCCCAAGGACCCCGGCGTAGGTGCGCAATTGGGTAAAGGTATCGATACCC 717
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Query 718      TTACGTGCGGCTTCGCGCACTCATGGGGTACATACCGCTCGTGGCGGCCCTCTTGGAG 777
                |||
Sbjct 718      TCAGTGGCGCTTCGCGCATCTCATGGGGTACATTCGCTCGTGGCGGCCCTTAGGGG 777
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Query 778      GCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGTTCTGGAAGACGCGGTGAACATGCAA 837
                |||
Sbjct 778      GCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGTTCTGGAAGACGCGGTGAACATGCAA 837
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Query 838      CAGGGAACCTTCTGTTGCTC-TTTCTCTATCTTCTTCTGGCCCTGCTCTCTTGCCCTG 896
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Sbjct 838      CAGGGAATCTGCCCCGTGCTCCTTT-TCTATCTTCTTTTGGCTTGGTCTCTGTTTG 896
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Query 897      ACTGTGCCC-GCTTCAGCCTACCAAGTGCAGCAAT-TCCTCGGG-GCTTTACCATGTACCC 953
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Sbjct 897      ACCAT-CCCAGCTTCCGCTTATGAAGTGCAGCAAGTA-TCGGAG-TGTACCATGTACAG 953
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Query 954      AATGATTGC-CCTAATCGAGTATTGTGTACGAGGCGGCCGA--TGCCATCCTGCACACT 1010
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Sbjct 954      AACGACTGCTCC-AACGCAAGCATTGTGTATGAGCGAGCGGACATG--ATCATGCATACC 1010
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Query 1011     CCGGGGTGTGT-CCCTTGCCTTCGCGAGGGTAACGCCCTCAGAGTGTGGGTGGCGGTGAC 1069
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Sbjct 1011     CCGGGGTGCGTGCCCT-GCGTTCGGGAGAACAACCTCTCCCGCTGCTGGGTAGCGCTAC 1069
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Query 1070     CCCACAGGTGGCCACGAGGACGGCAAAAC-TCCCAACAAC-CAGCTTCGACGTCATATC 1127
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Sbjct 1070     TCCCACGCTCGCGGCCAGGAACG-CTAGCGTCCCCACTACGAC-GATACGACGCCATGTC 1127
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Query 1128     GATCTGCTTGTGGGAGCGCCACC-CTCTGCTCGGCCCTCTACGTGGGGGACCTGTGCGG 1186
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Sbjct 1128     GATTTGCTCGTTGGG-GCGGCTGCTCTCTGCTCGGCTATGTACGTGGGAGATCTCTGCGG 1186
                |||
Query 1187     GTCTGCTCTTTCTT-GTTGGTCAACTGTTTACCTTCTCTCC-CAGGCGCCACTG-GACGAC 1243
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Sbjct 1187     ATCTGT-TTTCCTGCTCGCCAGCTGTTACCTTCTCGGCTC-GCCGGAC-GAGAC-A- 1241
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Query 1244     GCA-AG-ACTGCAATTGTTCTATCTATCCCGCCATATAACGGGTATCGCATGGCATGG 1301
                |||
Sbjct 1242     GTACAGGACTGCAATTGCTCAATATATCCCGGCCACGTGACAGGTCACCGTATGGCTTGG 1301
                |||
Query 1302     GATATGATGATGAACCTGGTCCCTACGCGAGCGTGTGGTGTAGCTCAGCTGCTCCGGATC 1361
                |||
Sbjct 1302     GATATGATGATGAACCTGGTACCTACAGAGCCCTAGTGGTATCGAGTTACTCCGGATC 1361
                |||
Query 1362     CCACAGGCTATCATGACATGATCGCTGGTGTCACTGGGGAGTCTTGGCGGGCATAGCG 1421
                |||
Sbjct 1362     CCACAGCTGTCTGGATATGGTGGCGGGGGCCATTGGGGAGTCTTAGCGGGCCTTGGC 1421
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Query 1422     TATT-TCCCATGGTGGGGAACCTGGGCGAAGGTCTCGTAGTGCTGCTGCTATTTGCCGG 1480
                |||
Sbjct 1422     TACTAT-TCCATGGTGGGGAACCTGGGCTAAGGTTCTGATTGTGATGCTACTCTTTGCCGG 1480
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Query 1481     CGTCGACGCGGAAACCCACGTCACCGGGGGAAATGCCGGCCGCAC-CACGGCT-GGCGTT 1538
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Sbjct 1481     CGTTGACGGGGAACTATGTGACAGGGGGGAC-GATGGCCAAAACACC-CTCGGGATT 1538
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Query	1539	--GTTGGTCTCCTTACACGAGCGCCAAGC-AGAACATCCAAC-TATCAACACCAACGG	1594
Sbjct	1539	ACGTCCCTCTT-TT-CACCCGG-GTCATCCAGAAAATCCAGTTG-TAAACACCAACGG	1594
Query	1595	CAGTTGGCAGATCAATAGCAGGCGCTTGAATTGCAATGAAAGCCTTAACACGCGGTGG-T	1653
Sbjct	1595	CAGCTGGCAGATCAACAGGACTGCCCTGAACAGCAATGACTCCCTCAACACTGGGTTCCT	1654
Query	1654	TAGCAGGGCTCTTCTATCAA-CACAAATTCAACTCTTCAGGCTGTCTGAGAGGTTGGCC	1712
Sbjct	1655	T-GCTGCGCTGTTCTA-CGTGCACAAGTTCAACTCATCTGGATGCCAGAGCGCATGGCC	1712
Query	1713	AGCTGCCGACGCGCTT--AC-CGATTTTGCCAGGGGTGGGGTCCATCAGTTATGCCAAC	1769
Sbjct	1713	AGCTGCAGCC--CATCGACGCG-TTC-GCTCAGGGGTGGGGGCCATCACTTA--C-AAT	1766
Query	1770	G-G--A-AGCGGCTCG-ACGA-ACGCCCTACTGCTGGCACTACCCCTCAAGACCTTGT	1823
Sbjct	1767	GAGTACA-CAGC-TCGGACCAGAGGCT-TATTGTTGGCACTACGACCCCGCGTGC	1823
Query	1824	GGCATTGTGCCCCCAAAG-AGCGTGTGTGGCCGGTATATTGCTTCACTTCCCA-GCCCGG	1881
Sbjct	1824	GGTATCGTACC CGCGCGCAG-GTGTGTGGTCCAGTGACTGCTTCACT-CCCAAGCCCTG	1881
Query	1882	TGTTGGTGGGAACGACCGCAGGT-CGGGCG-CGCGCTACCTACAGTGGGTGCA-AATG	1938
Sbjct	1882	TCGTTGGTGGGACGACCGACCGGTTCCG-CGTC-CCTACGTACAGTGGGGGG-AGAATG	1938
Query	1939	ATACGGATGT-CITCTGCTTAAACAACAC-CAGGCCACCGCTGGGCAATTGGTTCGGTTG	1996
Sbjct	1939	AGACGGAGCTGCTGCTTC-TTAAACAACAGC-GGCCCGCCGAAGCACTGGTTGGCTG	1996
Query	1997	TACCTGGATGAAC--CAACTGGATTCAACAA-AGTGTGGGAGCGCCCGCTTGTGT--C	2051
Sbjct	1997	TACATGGATGAA-TAGCA-CTGGGTTCAACAAGC-GTGGGGG-GCCCGCC-GTGTAA	2051
Query	2052	ATCGGAGGGG-TGGGCAACAACACCTTG-CTCTGCCCCACTGATTGCTTCGCAAAACATC	2109
Sbjct	2052	ATCGG-GGGGATCGGCAATAAAACCTTGAC-CTGCCCCACGGACTGCTTCGGAAGCACC	2109
Query	2110	CGGAAGCCACATACTCTCG-GTGGCGCTCCGCTCCCTGGATT-ACACCCAGGTGCATGTT	2167
Sbjct	2110	CCGAGGCCACTTACAC-CAAGTGTGGTTCGGGGCTTGG-TTGACACCCAGATGCTTGGT	2167
Query	2168	GCACTACCCGATAGGCTTTGGCACTATCCTTGTACCATCAA-TTACCATATTTCAAAG	2226
Sbjct	2168	CCACTACCCATACAGGCTTTGGCACTACCCCTGCACGTGCAACTTT-ACCATCTTCAAG	2226
Query	2227	TCAGGATGTACGTGGGAGGG-GTCGAGCAGAGCTGGAAGCGGCTGCAACTGGAGCGGG	2285
Sbjct	2227	TTAGGATGTACGTGGG-GGGAGTGGAGCAGAGCTCGAAGCGCATGCAATTGGACTCGA	2285
Query	2286	GGCGAAGCTGTGATCTGGAAGACAGGGACAGGTCGAGCTACGCCCCGTTGCTGCTGTC	2345
Sbjct	2286	GGAGAGCGTGTGAACCTGGAGGACAGGACAGATCAGAGCTTAGCCCGCTGCTGCTGCT	2345
Query	2346	ACCACACAGTGGCAGGTCTT-CCGTGTTCTTTACAGCCCTGCCAGC-CTTGTCACCG	2403
Sbjct	2346	ACAACGGAGTGGCAGGTA-TTGCCCTGTTCTTACACCCCTACCGGCTCT-GTCCACTG	2403
Query	2404	GCCTCATCCCTTCCACCAAGACATTGTGGACGTGCAGTACTTGTACGGGGTAGGGTCAA	2463
Sbjct	2404	GTTTGATCCATCTCCATCAGAACGTCGTGGAGCTACAACTGTACGGTATAGGGTCG-	2462
Query	2464	GCA-TCG-CGTCTGGGCCATTAAAGTGGGAGTACGTCGT-TCTCTGTTCTCTTCTGTTG	2520
Sbjct	2463	GCGGTGTG-TCTCTTGAATCAAAATGGGAGTATGCTCTGT-TGCTCTCTCTTCTTGG	2520
Query	2521	CAGACGCGCGCTGTGCT-CCTGCTTGTGGATGATGTTACTCATATCCCAAGCGGAGGCG	2579
Sbjct	2521	CGGACGCGCGGCTG-TGCTGCTTGTGGATGATGCTGCTGATAGCTCAAGCTGAGGCC	2579
Query	2580	GCTTTGGAGAACCTGTAATACTCAATGCAGCATCCCTGGCCGGGACGCACGGTC-TTGT	2638
Sbjct	2580	GCCCTAGAGAACCTGTGTGCTCTCAACGCGGACATCCGTGGCCGGGGCGCATGG-CATTCT	2638

Query	2639	GTCCTTCCTCGTGTCTTCTGCTT-TGCGTGGTATC-TGAAGGGTAGG-TGGGTGCCC-G	2694
Sbjct	2639	CTCCTTCCTCGTGTCTTCTG-TGCTGCCCTGGTA-CATCAAGGCGAGGCTGG-T-CCCTG	2694
Query	2695	GAGCGGTG-TACGCCCTCTACGG-GATGTGGCTCTCTCTGCTCTGCTGCGGTGGC	2752
Sbjct	2695	GGGCGG-CATATGCCCTCTACGGG-TATGGCCGCTACTCTGCTCTGCTGCGGTATAC	2752
Query	2753	TC-AGCGGGCATACGC-ACTGGACACGG-AGGTGGCCGCTCGTGTGGCGCGTGTGTTCT	2809
Sbjct	2753	ACCA-CGAGCATACGCCA-TGGAC-CGGGAGATGGCAGCATCGTGGGAGGCGCGGT-T	2808
Query	2810	T-GTCGGGT-TAATGGCGCT-GACTCT-GTCGCCATATTACAAGC-GCTATATCAGCT-G	2863
Sbjct	2809	TCGTAGG-TCGTGATA-CTCTTGAC-CTGTGACCGGCACTATAAGCTGTGTC-TC-GCTAG	2863
Query	2864	G-TGCATGTGGTGGCTT-CAGTATTTCTGACCAGAGTAGAAGCGCAACT-GCAGGTGTG	2920
Sbjct	2864	GCT-CATATGGTGG-TTACAATATTTTATCACCAGGGCCGAGGCACA-CTTGCAAGTGTG	2920
Query	2921	GGTTCccccccCAACAGTCCgggggggCGCGATGCCGTCACTTACTCATGTGTGT-AG	2979
Sbjct	2921	GATCCCCCCCCCAACGTTCCGGGGGGCGCGATGCCGTCACTTCTCAGCTGCGCGA-	2979
Query	2980	TACACCC-GACCCCTGGTATTTGAC-ATCACCAACTACTC-CTGGCCAT-CTTCGGACCC	3035
Sbjct	2980	TCACCCAGAGC-TAATCTTT-ACCATCACCAAAAT-CTTGCTCGCATACT-CGGTCCA	3035
Query	3036	CTT-TGGATTCTTCAAGCCAGTTTG-CTTAAAGTCCCTACTTCGTGCGCGTTCAAGGCC	3093
Sbjct	3036	CTCATGG-TGCTCCAGGCTGGTATAACC-AAAGTGGCGTACTTCGTGCGCGCACAGGCG	3093
Query	3094	TTT-TCCG-G-ATCTGCGCGCTAGCGCGGAAGATAGCCGGAGGTCAATTACGTGCAAAATGG	3150
Sbjct	3094	T-CATTCTGTGAT--GCATGCTGGTGCAGGAAGTGTGCTGGGGGTCAATATGTCCAAATGG	3150
Query	3151	C-CATCATCAAGTTAGGG-GCGCTTACTGGCACCTATGTGTATAAACCATCTCACCCCTCT	3208
Sbjct	3151	CTC-TCATGAAGTT-GGCCGCACTGACAGGTACGTACGTTTATGACCATCTCACCCCACT	3208
Query	3209	TCGAGACTGGGCGCACAACGG-CCTGCGAGATCTGGCCGTGGCTGTGGAAACAGTCGTCT	3267
Sbjct	3209	GCGGGACTGGGCGCCAGC-CGGGCTACGAGACTTTCGGTGGCAGTTGTAGCCCGTCGTCT	3267
Query	3268	TCTCCGA-ATGGAGACCAAGCTCATCAGTGGGGGGCAGATACCGCCGCTGCGGTGAC	3326
Sbjct	3268	TCTCT-GATATGGAGACCAAGTTATCACTGGGGGGCAGACCGCGCGCTGTGGGGAC	3326
Query	3327	ATCATCAACGGCTTTGCCGTCTCTGCCCTAGGGGCCAGG-AGATAC-TGCTTGGG-CCA	3383
Sbjct	3327	ATCATCTTGGGCTTGCCGTCTCCGCCCGCAGGGGG-AGGGAGATACAT-CT-GGGACCG	3383
Query	3384	GCCGACGGAAATGGTCTC-CAAGGGGTGGAGGTGTGCTGGCGCCCATCAGCGCGTACGCCCA	3442
Sbjct	3384	GCAGACAGCCTTGAAGGGCA-GGGGTGGGACTCTCTCGCGCTATTACGGGCTACTCCCA	3442
Query	3443	GCAGACGAGAGGCTCTTAGGGTGTATAATCACCAGCCTGACTGGCCGGGACAAAAACCA	3502
Sbjct	3443	ACAGACGCGAGGCTACTTGGCTGCATCATCTAGCTCACAGGCGGGGACAGGAACCA	3502
Query	3503	AGTGAGGGGTGAGGTCCA-GATCGTGTCAACTGTACCCAAACCTTCCTGGCAACGTGCA	3561
Sbjct	3503	GGTCGAGGGGGAGGTCCAAG-TGGTCTCCACGCAACACAATCTTCTTGGCGACCTTGGG	3561
Query	3562	TCAATGGGGTATGCTGGACTGTCTACCACGGGGCGGAAGCAGGACCATCGCATACCCA	3621
Sbjct	3562	TCAATGGCGTGTGTGGACTGTCTATCATGTTGCCGCTCAAAGACCTTGGCGG-CCCA	3620
Query	3622	A-GGGTCCTGTATCCAGATGTATACCAATGTGGACCAAGACCTTGTGGGTGGCCCGCT	3680
Sbjct	3621	AAGGGCCCAATCACCACAAATGTACACCAATGTGGACCAAGGACCTCGTGGCTGGCAAGG	3680
Query	3681	CCTCAAGTTCCCGCTCATTGACACCCTGTACCTGCGGCTCCTGGACCTTTACCTGTGTC	3740
Sbjct	3681	CCCCCGGGGCGGTTCTTTGACCCATGCACCTGCGGCGAGCTCGGACCTTTACTTGGTC	3740

Query	3741	ACGAGGACACCGCGATGTCATTCCCGTGCGCCGCGAGGTATAGACAGGGGTAGCCTGCTT	3800
Sbjct	3741	ACGAGGCAATGCCGATGTCATTCCCGTGCGCCGCGGGCGACAGCAGGGGGAGCCTACTC	3800
Query	3801	TCGCCCC-GGCCCAATTTCTACTTGAAAGGCTCCTCGGGGGTCCGCTGTTGTGCCCCG	3859
Sbjct	3801	TC-CCCCAGGCCGCTCTCTACTTGAAGGGCTCTTCGGGCGGTCCACTGCTCTGCCCCCTC	3859
Query	3860	GGGACACGCGGTGGGCCTATT-CAGGGCCGCGGTGTGCACCCGTGGAGTGGCTAAAGCGG	3918
Sbjct	3860	GGGGACAGCTGTGGGCATCTTTC-GGGCTGCCGTGTGCACCCGAGGGGTTCGAAGGCGG	3918
Query	3919	TGGACTTTAT-CCCTGTGGAGAACCTAGGGACAACCA-T--GAGATCCCCGGTGTTACAG	3974
Sbjct	3919	TGGACTTTGTATGCC-GTCCAGT-C-TATGGA-AACCATATGCGGTCCTCCCGCTCTACAG	3974
Query	3975	GACAATCTCTCTCCACGAGCTGCCCGAGAG-ITTCAGTGGGCGCACTGCATGCTTCC	4033
Sbjct	3975	GACAATCTGTCCCTCCGGCCGTACCGCAGA-CATTCAGTGGGCCATCTACACG-CC	4032
Query	4034	C-ACCGGCAGCGGTAAGAGCACCAGGTGCCGGCTGCGTAGCAGCCCA-GGGCTACAAG	4091
Sbjct	4033	CTACTGGTAGCGGAAGAGCACTAAGTGTCCGGCTGCGTAGTCAGCCCAAGG-TATAAG	4091
Query	4092	GTG-TTGGTGCTCAACCCCTCTGTTGCTGCAACGCTGGGCTTT-GGTGTTACATGTCCA	4149
Sbjct	4092	GTGCTTG-TCTGAACCCGTCGCTGCCGCCACCTAGG-TTCGGGGCGTATATGTCTA	4149
Query	4150	AGGCCCATGGGGTGTATCCTTAATATCAGGACCGGGGTGAGAACAAITACCCTGGCAGCC	4209
Sbjct	4150	AGGCACATGGTATCGACCTTAACATCAGAACCGGGGTAAAGACCATACCACGGGT-GCC	4208
Query	4210	CC-ATCAGTACTCCACTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCAGGAGGTGCT	4268
Sbjct	4209	CCCATCAGTACTCCACTATGGCAAGTTTCTTGCCGACGGTGGTTGCTCTGGGGGGCC	4268
Query	4269	TATGACATAATAATTTGTGACGAGTGCCACTCCACGGA-T-G-CCACATCCATCTTGGGC	4325
Sbjct	4269	TATGACATCATAATATGTGATGAGTGCCACTCAACTGACTCGACAC-T-ATCCTGGGC	4325
Query	4326	ATCGGCACGTGCTTGTACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACT	4385
Sbjct	4326	ATCGGCACAGTCTGGGACCAAGCGGAGCGGCTGGAGCGGACACTCGTCTGCTCGCCACC	4385
Query	4386	GCTACCCCTTCGGGACTCCGTCTGCTGTGTC-CATCTCAACATCGAGGAGTTGTCTGTCT	4444
Sbjct	4386	GCTACGCCCTCGGGATCGGTACCGGTG-CACATCCAAACATCGAGGAGTGGCTGTGTC	4444
Query	4445	CACCACCGGAGAGATCCCCTTTTATGCCTAAGGCTATCCCCCTCGAGGTGATCAAGGGGGG	4504
Sbjct	4445	CAGCACTGGAGAAATCCCCTTTTATGGCAAGGCATCCCCATCGAGACCAATCAAGGGGGG	4504
Query	4505	AAGACATCTCATCTTTCTGCCACTCAAAGAAGAAGTGCACGAGTCGCCGCGAAGCTGGT	4564
Sbjct	4505	GAGGCACCTCATTTTTCTGCCATTCCAAGAAGAAATGTGATGAGCTCGCGCGAAGCTG-T	4563
Query	4565	C-G-CATTGGGCATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGCTGTGATCCCG	4622
Sbjct	4564	CCGGCTTCGGAC-TCAATGCTGTAGCATATTACCGGGGCCCTGTATGTATCCGTATACCA	4622
Query	4623	ACCAGCGGCGATGTTGTGCTGCTG-TGTCACCGATGCTCTCATGACTGGCTTACCGGCGA	4681
Sbjct	4623	ACTAGCGGAGACGTCATTGTCTGTAG-CAACGGACGCTCTAATGACGGGCTTACCGGCGA	4681
Query	4682	CTTCGACTCTGTGATAGACTGCAACAGTGTTGTCACCTCAGACAGTCGATTTACGCCTTGA	4741
Sbjct	4682	TTTCGACTCAGTGATGCAATGCAATACATGTGTACCCAGACAGTCGACTTCAGCCTTGA	4741
Query	4742	CCCTACCTTTACCAATGAGACACAC-GTCCCCAGGATGCTGCTCCAGGACTCA-A	4799
Sbjct	4742	CCCGACCTTCAACATTGAGACGACGACCG-TGCCACAAGACGCGGTGTC-ACG-CTCGCA	4798
Query	4800	-CGCCGGGACGAGTGGCAGGGG 4822	
Sbjct	4799	GCGCGAGGACGAGTGGTAGGGG 4822	

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